

## SEQUENCE LISTING

&lt;110&gt; Jian Ni et al.

&lt;120&gt; Cytostatin II

&lt;130&gt; PF221D1

&lt;150&gt; 09/043,646

&lt;151&gt; 1998-09-09

&lt;150&gt; PCT/US95/12540

&lt;151&gt; 1995-09-25

&lt;160&gt; 8

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; human

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (16) .. (411)

&lt;223&gt;

&lt;400&gt; 1

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gggggaaaggg caagg atg gtg gag gct ttc tgt gct acc tgg aag ctg acc      51
                Met Val Glu Ala Phe Cys Ala Thr Trp Lys Leu Thr
                  1                      5                      10

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aac agt cag aac ttt gat gag tac atg aag gct cta ggc gtg ggc ttt      99
Asn Ser Gln Asn Phe Asp Glu Tyr Met Lys Ala Leu Gly Val Gly Phe
    15                      20                      25

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gcc act agg cag gtg gga aat gtg acc aaa cca acg gta att atc agt      147
Ala Thr Arg Gln Val Gly Asn Val Thr Lys Pro Thr Val Ile Ile Ser
    30                      35                      40

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caa gaa gga gac aaa gtg gtc atc agg act ctc agc aca ttc aag aac      195
Gln Glu Gly Asp Lys Val Val Ile Arg Thr Leu Ser Thr Phe Lys Asn
    45                      50                      55                      60

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acg gag att agt ttc cag ctg gga gaa gag ttt gat gaa acc act gca      243
Thr Glu Ile Ser Phe Gln Leu Gly Glu Glu Phe Asp Glu Thr Thr Ala
    65                      70                      75

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gat gat aga aac tgt aag tct gtt gtt agc ctg gat gga gac aaa ctt      291
Asp Asp Arg Asn Cys Lys Ser Val Val Ser Leu Asp Gly Asp Lys Leu
    80                      85                      90

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gtt cac ata cag aaa tgg gat ggc aaa gaa aca aat ttt gta aga gaa      339
Val His Ile Gln Lys Trp Asp Gly Lys Glu Thr Asn Phe Val Arg Glu
    95                      100                      105

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att aag gat ggc aaa atg gtt atg acc ctt act ttt ggt gat gtg gtt      387
Ile Lys Asp Gly Lys Met Val Met Thr Leu Thr Phe Gly Asp Val Val
    110                      115                      120

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gct gtt cgc cac tat gag aag gca taaaaatgtc cctgggtcggg gcttggaaga 441  
 Ala Val Arg His Tyr Glu Lys Ala  
 125 130

gctcttcagt ttttctgttt cctcaagtct cagtgtctatc ctattacaac atggctgac 501  
 attaattaga aggttatcct tgggtgtggag gtggaaaatg gtgatttaaa aacttggtac 561  
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 20 25 30

Val Gly Asn Val Thr Lys Pro Thr Val Ile Ile Ser Gln Glu Gly Asp  
 35 40 45

Lys Val Val Ile Arg Thr Leu Ser Thr Phe Lys Asn Thr Glu Ile Ser  
 50 55 60

Phe Gln Leu Gly Glu Glu Phe Asp Glu Thr Thr Ala Asp Asp Arg Asn  
 65 70 75 80

Cys Lys Ser Val Val Ser Leu Asp Gly Asp Lys Leu Val His Ile Gln  
 85 90 95

Lys Trp Asp Gly Lys Glu Thr Asn Phe Val Arg Glu Ile Lys Asp Gly  
 100 105 110

Lys Met Val Met Thr Leu Thr Phe Gly Asp Val Val Ala Val Arg His  
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Tyr Glu Lys Ala  
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52

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